

*AMENDMENTS TO THE CLAIMS*

This listing of claims replaces all prior versions, and listings, of claims in the application.

1. (currently amended) A composition for the inhibition of the translation of a Mect1-MAML2 chimeric gene, consisting essentially of: (a) a fragment of the nucleic acid encoding ~~the a~~ Mect1-MAML2 gene protein of SEQ ID NO: 12, and (b) a nucleic acid complementary to the fragment, wherein the fragment is about 17 to about 32 nucleotides in length.
2. (original) The composition of claim 1, wherein the nucleic acid molecule complementary to the fragment has from 1 to about 10 base substitutions, and wherein the nucleic acid molecule complementary to the fragment optionally contains one or more insertions and is about 19 to about 35 nucleotides in length.
3. (currently amended) The composition of claim 2, ~~further consisting essentially of a restriction enzyme sequence~~, wherein the fragment and the nucleic acid complementary to the fragment are joined by ~~the a~~ nucleic acid sequence recognized by a restriction enzyme sequence.
4. (currently amended) The composition of claim 1, wherein the ~~Mect1-MAML2 gene has~~ fragment of a nucleic acid encoding the Mect1-MAML2 protein of SEQ ID NO: 12 is a fragment of a nucleic acid having the nucleotide sequence of SEQ ID NO: 1.
5. (original) The composition of claim 1, wherein the Mect1-MAML2 chimeric gene results from a t(11;19) translocation.
6. (original) The composition of claim 2, wherein the fragment has the nucleotide sequence of SEQ ID NO: 5 or 6.
7. (withdrawn) The composition of claim 6, wherein the nucleic acid complementary to the fragment has the nucleotide sequence of SEQ ID NO: 7.
8. (currently amended) The composition of claim 1, wherein the ~~composition~~ fragment, the nucleic acid complementary to the fragment, or both are is in a vector.

9. (original) The composition of claim 8, wherein the vector is a plasmid.
10. (original) The composition of claim 8, wherein the vector is a viral vector.
11. (original) The composition of claim 10, wherein the viral vector is an adenoviral vector.
12. (original) The composition of claim 3, wherein the fragment is about 21 to about 32 nucleotides in length.
13. (original) The composition of claim 12, wherein the fragment is about 28 to about 29 nucleotides in length.
14. (currently amended) The composition of claim 3, wherein the restriction enzyme sequence is a *Hin dIII* sequence.
15. (original) The composition of claim 2, wherein the nucleic acid molecule complementary to the fragment has from about 2 to about 5 substitutions.
16. (original) The composition of claim 1, wherein the composition has the nucleotide sequence of SEQ ID NO: 2, 3, or 4.
17. (withdrawn) The composition of claim 1, wherein the fragment has the nucleotide sequence of SEQ ID NO: 8 or 9.
18. (original) The composition of claim 1, wherein the fragment is about 17 to about 22 nucleotides in length.
19. (original) The composition of claim 18, wherein the fragment is about 19 to about 21 nucleotides in length.
20. (original) The composition of claim 1, wherein the fragment and the nucleic acid complementary to the fragment are under the control of different promoters on the same nucleic acid molecule.
21. (original) The composition of claim 20, wherein the promoters are RNA polymerase promoters.

22. (original) The composition of claim 21, wherein the promoters are RNA polymerase III promoters.

23. (original) The composition of claim 1, wherein, upon annealing of the transcripts of the fragment and the nucleic acid complementary to the fragment, the annealed transcripts of the composition have a 3' overhang consisting of 1 to about 4 nucleotides on one or both ends of the annealed transcripts.

24. (original) The composition of claim 23, wherein the 3' overhang consists of about 2 to about 3 nucleotides.

25. (original) The composition of claim 23, wherein one or more of the nucleotides of the 3' overhang are uridine.

26. (original) The composition of claim 23, wherein the 3' overhang consists of 2 uridine residues.

27.-34. (canceled)

35. (new) The composition of claim 4, wherein the fragment and the nucleic acid complementary to the fragment are joined by a nucleic acid sequence recognized by a restriction enzyme.

36. (new) The composition of claim 4, wherein the fragment, the nucleic acid complementary to the fragment, or both are in a vector.

37. (new) The composition of claim 4, wherein the nucleic acid molecule complementary to the fragment has from about 2 to about 5 substitutions.

38. (new) The composition of claim 4, wherein the fragment and the nucleic acid complementary to the fragment are under the control of different promoters on the same nucleic acid molecule.

39. (new) The composition of claim 4, wherein, upon annealing of the transcripts of the fragment and the nucleic acid complementary to the fragment, the annealed transcripts of the

composition have a 3' overhang consisting of 1 to about 4 nucleotides on one or both ends of the annealed transcripts.

40. (new) A composition for the inhibition of the translation of a Mect1-MAML2 chimeric gene, consisting essentially of: (a) a fragment of the nucleic acid encoding a Mect1-MAML2 chimeric gene, wherein the nucleic acid has about 90% homology or greater with the nucleic acid sequence of SEQ ID NO: 1, and (b) a nucleic acid complementary to the fragment, wherein the fragment is about 17 to about 32 nucleotides in length.

41. (new) The composition of claim 40, wherein the nucleic acid has about 95% or greater homology with the nucleic acid sequence of SEQ ID NO: 1.

42. (new) The composition of claim 40, wherein the fragment and the nucleic acid complementary to the fragment are joined by a nucleic acid sequence recognized by a restriction enzyme.

43. (new) The composition of claim 40, wherein the fragment, the nucleic acid complementary to the fragment, or both are in a vector.

44. (new) The composition of claim 40, wherein the nucleic acid molecule complementary to the fragment has from about 2 to about 5 substitutions.

45. (new) The composition of claim 40, wherein the fragment and the nucleic acid complementary to the fragment are under the control of different promoters on the same nucleic acid molecule.

46. (new) The composition of claim 40, wherein, upon annealing of the transcripts of the fragment and the nucleic acid complementary to the fragment, the annealed transcripts of the composition have a 3' overhang consisting of 1 to about 4 nucleotides on one or both ends of the annealed transcripts.